WHAT IS CLAIMED IS:

1. An isolated nucleic acid comprising a sequence as set forth in SEQ ID NO:1 and variants thereof having at least 70% identity to SEQ ID NO:1 and encoding a polypeptide having polymerase activity at a temperature in a range from about 90°C to 113°C.

2. The isolated nucleic acid of claim 1, wherein the polymerase activity is retained at the temperature for four or more hours.

3. The isolated nucleic acid of claim 1, comprising a sequence as set forth in SEQ ID NO: 1, sequences substantially identical thereto, and sequences complementary thereto.

4. An isolated nucleic acid that hybridizes to a nucleic acid of claim 1 under conditions of high stringency.

5. An isolated nucleic acid that hybridizes to a nucleic acid of claim 1 under conditions of moderate stringency.

6. An isolated nucleic acid that hybridizes to a nucleic acid of claim 1 under conditions of low stringency.

7. An isolated nucleic acid having at least 70% homology to the nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm.

8. An isolated nucleic acid having at least 80% homology to the nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm.

9. An isolated nucleic acid having at least 90% homology to the nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm.

10. An isolated nucleic acid having at least 95% homology to the nucleic acid of claim 1 as determined by analysis with a sequence comparison algorithm.

11. The isolated nucleic acid of claim 7, 8, 9, or 10, wherein the sequence comparison algorithm is FASTA version 3.0t78 with the default parameters.

12. An isolated nucleic acid comprising at least 10 consecutive bases of a sequence as set forth in SEQ ID NOs: 1, sequences substantially identical thereto, and sequences complementary thereto.

13. An isolated nucleic acid having at least 70% homology to the nucleic acid of claim 11 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

14. An isolated nucleic acid having at least 80% homology to the nucleic acid of claim 11 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

15. An isolated nucleic acid having at least 90% homology to the nucleic acid of claim 11 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

16. An isolated nucleic acid encoding a polypeptide having a sequence as set forth in SEQ ID NO:2, and sequences substantially identical thereto.

17. An isolated nucleic acid encoding a polypeptide comprising at least 10 consecutive amino acids of a polypeptide having a sequence selected from the group consisting of SEQ ID NO: 2, and sequences substantially identical thereto.

18. A purified polypeptide having at least 70% homology to the polypeptide of claim 16 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

19. A purified polypeptide having at least 80% homology to the polypeptide of claim 16 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

20. A purified polypeptide having at least 90% homology to the polypeptide of claim 16 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

21. A purified polypeptide having at least 95% homology to the polypeptide of claim 16 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

22. A purified polypeptide having at least 70% homology to the polypeptide of claim 17 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

23. A purified polypeptide having at least 80% homology to the polypeptide of claim 17 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

24. A purified polypeptide having at least 90% homology to the polypeptide of claim 17 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

25. A purified polypeptide having at least 95% homology to the polypeptide of claim 17 as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

26. A purified polypeptide having a sequence as set forth in SEQ ID NO: 2, and sequences substantially identical thereto, wherein the polypeptide has polymerase activity at temperatures in the range from about 70°C up to about 113° C.

27. A purified antibody that specifically binds to a polypeptide having a sequence as set forth in SEQ ID NO: 2, and sequences substantially identical thereto.

28. A purified antibody that specifically binds to a polypeptide having at least 10 consecutive amino acids of one of the polypeptides of SEQ ID NO: 2, and sequences substantially identical thereto.

29. A method of producing a polypeptide having a sequence as set forth in SEQ ID NO: 2, and sequences substantially identical thereto, comprising introducing a nucleic acid encoding the polypeptide into a host cell under conditions that allow expression of the polypeptide and recovering the polypeptide.

30. A method of producing a polypeptide comprising at least 10 amino acids of a sequence as set forth in SEQ ID NO: 2, and sequences substantially identical thereto comprising introducing a nucleic acid encoding the polypeptide, operably linked to a promoter, into a host cell under conditions that allow expression of the polypeptide and recovering the polypeptide.

31. A method of generating a variant comprising:

obtaining a nucleic acid comprising a sequence as set forth in SEQ ID NO: 1, sequences substantially identical thereto, sequences complementary thereto, fragments comprising at least 30 consecutive nucleotides thereof, and fragments comprising at least 30 consecutive nucleotides of the sequences complementary to SEQ ID NO: 1 and

modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence.

32. The method of claim 31, wherein the modifications are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, ligation reassembly, GSSM and any combination thereof.

33. The method of claim 31, wherein the modifications are introduced by error-prone PCR.

34. The method of claim 31, wherein the modifications are introduced by shuffling.

35. The method of claim 31, wherein the modifications are introduced by oligonucleotide-directed mutagenesis.

36. The method of claim 31, wherein the modifications are introduced by assembly PCR.

37. The method of claim 31, wherein the modifications are introduced by sexual PCR mutagenesis.

38. The method of claim 31, wherein the modifications are introduced by *in vivo* mutagenesis.

39. The method of claim 31, wherein the modifications are introduced by cassette mutagenesis.

40. The method of claim 31, wherein the modifications are introduced by recursive ensemble mutagenesis.

41. The method of claim 31, wherein the modifications are introduced by exponential ensemble mutagenesis.

42. The method of claim 31, wherein the modifications are introduced by site-specific mutagenesis.

43. A computer readable medium having stored thereon a nucleic acid sequence as set forth in SEQ ID NO: 1, and sequences substantially identical thereto, or a polypeptide sequence as set forth in SEQ ID NO: 2, and sequences substantially identical thereto.

44. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a nucleic acid sequence as set forth in SEQ ID NO: 1, and sequences substantially identical thereto, or a polypeptide sequence as set forth in SEQ ID NO: 2, and sequences substantially identical thereto.

45. The computer system of claim 43, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

46. The computer system of claim 44, wherein the sequence comparison algorithm comprises a computer program which indicates polymorphisms.

47. The computer system of claim 43, further comprising an identifier which identifies features in said sequence.

48. A method for comparing a first sequence to a reference sequence wherein said first sequence is a nucleic acid sequence as set forth in SEQ ID Nos: 1, and sequences substantially identical thereto, or a polypeptide sequence as set forth in SEQ ID NO: 2, and sequences substantially identical thereto comprising:

reading the first sequence and the reference sequence through use of a computer program which compares sequences; and

determining differences between the first sequence and the reference sequence with the computer program.

49. The method of claim 47, wherein determining differences between the first sequence and the reference sequence comprises identifying polymorphisms.

50. A method for identifying a feature in a sequence wherein the sequence is as set forth in SEQ ID NO: 1, sequences substantially identical thereto, or a polypeptide sequence of SEQ ID NO: 2, and sequences substantially identical thereto comprising:

reading the sequence through the use of a computer program which identifies features in sequences; and

identifying features in the sequences with the computer program.

51. An assay for identifying functional polypeptide fragments or variants encoded by fragments of SEQ ID NO: 1, and sequences substantially identical thereto, that retain the polymerase function of the polypeptide of SEQ ID NO: 2, and sequences substantially identical thereto, said assay comprising:

utilizing a polypeptide encoded by a nucleic acid having at least 70% homology to SEQ ID NO: 1, and sequences substantially identical thereto, or polypeptide fragment or variant encoded by SEQ ID NO: 1, to effect DNA polymerase activity in a PCR amplification at extreme high temperature for four or more hours and under conditions that allow said polypeptide or fragment or variant to function, and

detecting formation of an amplification product, wherein formation of the amplification product is indicative of a functional DNA polymerase polypeptide or fragment or variant.